Kidney Disease ML Analytics

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Kidney Disease Analysis from gene expression profiles of 12 healthy and 4 renal disease samples for day 1, 3, 6, and 9 days in culture

https://www.ncbi.nlm.nih.gov/geo/download/?acc=GSE141257

```
kidneyDisease <- read.csv('Samples16-downloaded-kidney-disease.csv',
                          sep=',', header=TRUE,
                          na.strings=c('',' ','NA'))
head(kidneyDisease)
```

```
##          X X1_AK124p1_Adh.count X2_AK124p1_SPH3d.count
## 1     A1BG                   16                      8
## 2 A1BG-AS1                    2                      2
## 3     A1CF                    1                      0
## 4      A2M                    4                      1
## 5  A2M-AS1                    5                      9
## 6    A2ML1                    0                      0
##   X3_AK124p1_SPH6d.count X4_AK124p1_SPH9d.count X5_AK125p1_Adh.count
## 1                      3                      4                   26
## 2                      1                      2                    0
## 3                      2                      1                    0
## 4                      4                      5                    3
## 5                      4                      5                   14
## 6                      2                      0                    0
##   X6_AK125p1_SPH3d.count X7_AK125p1_SPH6d.count X8_AK125p1_SPH9d.count
## 1                     15                     18                     17
## 2                      5                      5                      2
## 3                      2                      1                      2
## 4                     14                     31                     33
## 5                     12                     20                     17
## 6                      3                      0                      1
##   AK82p2Adh AK82p3SPH3d AK82p3SPH6d AK82p3SPH10d AK86p1Adh AK86p2.SPH3d
## 1        16           9           9           11        36           25
## 2         8          12           4            8         9           10
## 3        12          11           9            8        20            8
## 4         2          68         126          103         2           52
## 5        31          45          26           25        24           18
## 6         6           3           2           11         1            2
##   AK86p2.SPH6d AK86p2.SPH10d
## 1           18            15
## 2           10             5
## 3            6             7
## 4          142           119
## 5           30            20
## 6            6             6
```

```
tail(kidneyDisease)
```

```
##            X X1_AK124p1_Adh.count X2_AK124p1_SPH3d.count
## 25364   ZXDC                  185                    157
## 25365 ZYG11A                   13                     12
## 25366 ZYG11B                  162                    122
## 25367    ZYX                 2369                   1408
## 25368  ZZEF1                  224                    275
## 25369   ZZZ3                  279                    198
##       X3_AK124p1_SPH6d.count X4_AK124p1_SPH9d.count X5_AK125p1_Adh.count
## 25364                    156                    159                  468
## 25365                      5                      8                   32
## 25366                    127                     98                  296
## 25367                   1171                   1263                 5406
## 25368                    267                    250                  507
## 25369                    216                    189                  490
##       X6_AK125p1_SPH3d.count X7_AK125p1_SPH6d.count X8_AK125p1_SPH9d.count
## 25364                    513                    487                  421
## 25365                     36                     31                   21
## 25366                    351                    410                  341
## 25367                   4665                   4875                 4272
## 25368                    821                    886                  669
## 25369                    561                    566                  508
##       AK82p2Adh AK82p3SPH3d AK82p3SPH6d AK82p3SPH10d AK86p1Adh
## 25364       867        1174        1321         1169       944
## 25365       186         122          98           67       151
## 25366       889        1246        1398         1197       554
## 25367      5560        6262        5831         5165      3920
## 25368      1324        1834        2090         2006      1036
## 25369      1304        1519        1889         1518       869
##       AK86p2.SPH3d AK86p2.SPH6d AK86p2.SPH10d
## 25364         1522         1587          1122
## 25365          106          113            65
## 25366         1294         1337          1072
## 25367         7483         6378          5735
## 25368         2076         2299          2028
## 25369         1691         1795          1389
```

```
SampleType <- read.csv('diseaseSampleType.csv', sep=',', header=TRUE,
                       na.strings=c('',' ', 'NA'))
```

```
SampleType
```

```
##        sample             sample_ID     Condition testCondition
## 1  GSM4200015            AK82p2Adh       healthy      adherent
## 2  GSM4200016          AK82p3SPH3d       healthy   3daySpheres
## 3  GSM4200017          AK82p3SPH6d       healthy   6daySpheres
## 4  GSM4200018         AK82p3SPH10d       healthy   9daySpheres
## 5  GSM4200019            AK86p1Adh       healthy      adherent
## 6  GSM4200020          AK86p2-SPH3d       healthy   3daySpheres
## 7  GSM4200021          AK86p2-SPH6d       healthy   6daySpheres
## 8  GSM4200022         AK86p2-SPH10d       healthy   9daySpheres
```

```
## 9  GSM4200023   1_AK124p1_Adh.count renal disease      adherent
## 10 GSM4200024 2_AK124p1_SPH3d.count renal disease   3daySpheres
## 11 GSM4200025 3_AK124p1_SPH6d.count renal disease   6daySpheres
## 12 GSM4200026 4_AK124p1_SPH9d.count renal disease   9daySpheres
## 13 GSM4200027   5_AK125p1_Adh.count       healthy      adherent
## 14 GSM4200028 6_AK125p1_SPH3d.count       healthy   3daySpheres
## 15 GSM4200029 7_AK125p1_SPH6d.count       healthy   6daySpheres
## 16 GSM4200030 8_AK125p1_SPH9d.count       healthy   9daySpheres
```

The sample_IDs with AK124p1 in the name are the four renal disease samples

```
colnames(kidneyDisease)
```

```
##  [1] "X"                       "X1_AK124p1_Adh.count"
##  [3] "X2_AK124p1_SPH3d.count" "X3_AK124p1_SPH6d.count"
##  [5] "X4_AK124p1_SPH9d.count" "X5_AK125p1_Adh.count"
##  [7] "X6_AK125p1_SPH3d.count" "X7_AK125p1_SPH6d.count"
##  [9] "X8_AK125p1_SPH9d.count" "AK82p2Adh"
## [11] "AK82p3SPH3d"            "AK82p3SPH6d"
## [13] "AK82p3SPH10d"           "AK86p1Adh"
## [15] "AK86p2.SPH3d"           "AK86p2.SPH6d"
## [17] "AK86p2.SPH10d"
```

```
healthy <- kidneyDisease[,-c(2:5)]
colnames(healthy)[1] <- 'Gene'
renalDisease <- kidneyDisease[,c(1,2:5)]
colnames(renalDisease) <- c('Gene','renal_0','renal_3','renal_6','renal_9')
```

```
colnames(healthy)
```

```
##  [1] "Gene"                    "X5_AK125p1_Adh.count"
##  [3] "X6_AK125p1_SPH3d.count" "X7_AK125p1_SPH6d.count"
##  [5] "X8_AK125p1_SPH9d.count" "AK82p2Adh"
##  [7] "AK82p3SPH3d"            "AK82p3SPH6d"
##  [9] "AK82p3SPH10d"           "AK86p1Adh"
## [11] "AK86p2.SPH3d"           "AK86p2.SPH6d"
## [13] "AK86p2.SPH10d"
```

```
dim(healthy)
```

```
## [1] 25369    13
```

```
colnames(renalDisease)
```

```
## [1] "Gene"    "renal_0" "renal_3" "renal_6" "renal_9"
```

```
dim(renalDisease)
```

```
## [1] 25369     5
```

```
str(healthy)
```

```
## 'data.frame':    25369 obs. of  13 variables:
##  $ Gene                  : Factor w/ 25369 levels "A1BG","A1BG-AS1",..: 1 2 3 4 5 6 7 8 9 10 ...
##  $ X5_AK125p1_Adh.count  : int  26 0 0 3 14 0 0 0 1031 2 ...
##  $ X6_AK125p1_SPH3d.count: int  15 5 2 14 12 3 0 0 1393 6 ...
##  $ X7_AK125p1_SPH6d.count: int  18 5 1 31 20 0 0 0 1365 3 ...
##  $ X8_AK125p1_SPH9d.count: int  17 2 2 33 17 1 0 0 1126 3 ...
##  $ AK82p2Adh             : int  16 8 12 2 31 6 0 2 939 2 ...
##  $ AK82p3SPH3d           : int  9 12 11 68 45 3 0 2 1043 1 ...
##  $ AK82p3SPH6d           : int  9 4 9 126 26 2 0 2 982 2 ...
##  $ AK82p3SPH10d          : int  11 8 8 103 25 11 1 1 1123 1 ...
##  $ AK86p1Adh             : int  36 9 20 2 24 1 0 3 626 3 ...
##  $ AK86p2.SPH3d          : int  25 10 8 52 18 2 0 2 1334 1 ...
##  $ AK86p2.SPH6d          : int  18 10 6 142 30 6 0 2 1493 2 ...
##  $ AK86p2.SPH10d         : int  15 5 7 119 20 6 0 2 909 7 ...
```

```
str(renalDisease)
```

```
## 'data.frame':    25369 obs. of  5 variables:
##  $ Gene   : Factor w/ 25369 levels "A1BG","A1BG-AS1",..: 1 2 3 4 5 6 7 8 9 10 ...
##  $ renal_0: int  16 2 1 4 5 0 0 0 536 0 ...
##  $ renal_3: int  8 2 0 1 9 0 0 0 436 1 ...
##  $ renal_6: int  3 1 2 4 4 2 0 0 378 1 ...
##  $ renal_9: int  4 2 1 5 5 0 0 0 352 0 ...
```

```
library(dplyr)
```

Assign no duplicate instances of genes

```
Renal_df <- renalDisease[!duplicated(renalDisease$Gene),]
```

Check that all the genes have 1 count each, they do

```
renalCounts <- Renal_df %>% group_by(Gene) %>%
               summarise(counts = n())
dim(renalCounts)
```

```
## [1] 25369     2
```

```
unique(renalCounts$counts)
```

```
## [1] 1
```

```
healthyCounts <- healthy %>% group_by(Gene) %>%
                    summarise(counts = n())
dim(healthyCounts)
```

```
## [1] 25369     2
```

```
unique(renalCounts$counts)
```

```
## [1] 1
```

Attach a field to the renal and healthy data frames for gene means

```
row.names(renalDisease) <- renalDisease$Gene
renalDisease <- renalDisease[2:5]
renalDisease$Gene_Means <- rowMeans(renalDisease)
```

```
row.names(healthy) <- healthy$Gene
healthy <- healthy[2:13]
healthy$Gene_Means <- round(rowMeans(healthy),3)
```

```
colnames(healthy)[13] <- "healthy_Means"
colnames(renalDisease)[5] <- "renal_Means"
```

```
Combined <- cbind(renalDisease, healthy)
Combined <- Combined[,c(5,18,1:4,6:17)]
```

Create the fold change field to compare the change in Renal diseased gene expression to healthy gene expression

```
Fold_Change <- Combined %>% mutate(Fold_Change = renal_Means/healthy_Means)
row.names(Fold_Change) <- row.names(Combined)
Fold_Change <- Fold_Change[,c(19,1:18)]
```

Remove NaN's or Not a number and Inf when dividing by zero or a very small value

```
Fold_Change$Fold_Change <- gsub('NaN',0,Fold_Change$Fold_Change)
Fold_Change$Fold_Change <- gsub('Inf', 0, Fold_Change$Fold_Change)
Fold_Change$Fold_Change <- round(as.numeric(Fold_Change$Fold_Change),3)
```

```
Top20_FC <- Fold_Change[order(Fold_Change$Fold_Change, decreasing=TRUE)[0:20],]
```

Create the Differential Expression in renal Disease compared to healthy genes

```
Differential <- Fold_Change %>% mutate(Differential_Expression = healthy_Means-renal_Means)
Differential <- Differential[,c(20,1:19)]
Differential$Differential_Expression <-       round(as.numeric(Differential$Differential_Expression, 3)
row.names(Differential) <- row.names(Fold_Change)
```

Since this is healthy - diseased, positive values mean the diseased gene expression means are lower than the healthy gene expression levels

```
downgraded <- Differential[order(Differential$Differential_Expression,
                                 decreasing=TRUE),]
```

Top 20 downgraded genes

```
Top20_down <- downgraded[0:20,]
```

Top 20 upgraded genes, diseased gene expression means were higher than the healthy gene expression means, hence negative values for differential expression

```
upgraded <- Differential[order(Differential$Differential_Expression,
                               decreasing=FALSE),]
```

```
Top20_up <- upgraded[0:20,]
```

```
Top20_up
```

```
##              Differential_Expression Fold_Change renal_Means healthy_Means
## XIST                           -1109    1109.750     1109.75         1.000
## CLDN2                           -428       1.264     2052.25      1624.167
## TDRD1                            -70       7.523       80.25        10.667
## CDKN1C                           -66       1.117      631.00       564.917
## CEBPD                            -33       1.031     1101.00      1067.750
## LOC101928796                     -32       5.812       38.75         6.667
## LBP                              -30       2.521       50.00        19.833
## LOC389332                        -29       1.143      234.25       205.000
## CA9                              -21       1.385       75.50        54.500
## B4GALNT4                         -19       1.447       61.00        42.167
## IFI27                            -18       1.149      142.25       123.833
## NAT8                             -16       2.169       30.00        13.833
## OVCH1-AS1                        -15      88.323       14.75         0.167
## ANGPTL3                          -14       1.933       29.00        15.000
## RARRES1                          -13       1.206       78.50        65.083
## CADM3                            -10       1.386       35.00        25.250
## PRR7                              -9       1.064      155.75       146.333
## FMO1                              -8       1.442       24.75        17.167
## PDF                               -8       1.160       59.75        51.500
## CFH                               -6       1.028      227.50       221.333
##              renal_0 renal_3 renal_6 renal_9 X5_AK125p1_Adh.count
## XIST            1083    1181    1072    1103                    1
## CLDN2            695    1922    2640    2952                  740
## TDRD1             88      84      90      59                    4
## CDKN1C          1034     493     517     480                  934
## CEBPD           2333     616     721     734                 4205
## LOC101928796      30      53      32      40                    3
## LBP              101      30      39      30                    3
## LOC389332        122     179     306     330                  158
## CA9              191      24      37      50                  118
```

```
## B4GALNT4          70      43      58      73                  40
## IFI27            110     154     161     144                  32
## NAT8               0      13      42      65                   3
## OVCH1-AS1         21      12      11      15                   1
## ANGPTL3            0      25      64      27                   0
## RARRES1          124      51      78      61                  75
## CADM3             17      22      43      58                  22
## PRR7             262     134     111     116                 439
## FMO1               3       5      36      55                   0
## PDF               43      53      59      84                  84
## CFH              202     178     265     265                 241
##             X6_AK125p1_SPH3d.count X7_AK125p1_SPH6d.count
## XIST                             1                      0
## CLDN2                         2256                   2530
## TDRD1                            3                      2
## CDKN1C                         604                    704
## CEBPD                         1926                   1957
## LOC101928796                    12                     15
## LBP                              5                      4
## LOC389332                      213                    310
## CA9                             15                     20
## B4GALNT4                        32                     44
## IFI27                          105                    116
## NAT8                            22                     34
## OVCH1-AS1                        0                      0
## ANGPTL3                         27                     47
## RARRES1                         57                     75
## CADM3                           27                     56
## PRR7                           319                    319
## FMO1                             9                     16
## PDF                            118                    160
## CFH                            139                    220
##             X8_AK125p1_SPH9d.count AK82p2Adh AK82p3SPH3d AK82p3SPH6d
## XIST                             1         2          1          1
## CLDN2                         2901       880        876       1553
## TDRD1                            3        21         14         25
## CDKN1C                         583       170        483        483
## CEBPD                         1832       301        255        344
## LOC101928796                     6         6          6          3
## LBP                             16         0          0          3
## LOC389332                      343        67        115        208
## CA9                             34       154         12         12
## B4GALNT4                        44        32         20         24
## IFI27                           95        94        180        175
## NAT8                            70         0          4          7
## OVCH1-AS1                        0         0          0          0
## ANGPTL3                         47         3          7         10
## RARRES1                         92        23         35        103
## CADM3                           74         4          5         15
## PRR7                           240        83         29         16
## FMO1                            26         0         10         10
## PDF                            147        10         10          2
## CFH                            194       604        230        145
##             AK82p3SPH10d AK86p1Adh AK86p2.SPH3d AK86p2.SPH6d
```

```
## XIST                    1         2           2           0
## CLDN2                2970       706        1420        2156
## TDRD1                  29         5           2          11
## CDKN1C                376       427         890         928
## CEBPD                 264       588         476         435
## LOC101928796            4         3          13           6
## LBP                    10        61          33         101
## LOC389332             321       149         221         262
## CA9                    25       177          27          35
## B4GALNT4               32        89          43          57
## IFI27                 196        71         187         153
## NAT8                   15         0           3           3
## OVCH1-AS1               0         0           0           1
## ANGPTL3                22         3           9           3
## RARRES1               115        66          35          63
## CADM3                  55        11           3          17
## PRR7                   43        82          79          69
## FMO1                   96         0           7           9
## PDF                    11         7          38          24
## CFH                   132       322         131         185
##              AK86p2.SPH10d
## XIST                     0
## CLDN2                  502
## TDRD1                    9
## CDKN1C                 197
## CEBPD                  230
## LOC101928796             3
## LBP                      2
## LOC389332               93
## CA9                     25
## B4GALNT4                49
## IFI27                   82
## NAT8                     5
## OVCH1-AS1                0
## ANGPTL3                  2
## RARRES1                 42
## CADM3                   14
## PRR7                    38
## FMO1                    23
## PDF                      7
## CFH                    113
```

```
Top20_down
```

```
##        Differential_Expression Fold_Change renal_Means healthy_Means
## EEF1A1                  210936       0.187    48649.75     259585.25
## SPP1                    168566       0.310    75657.25     244223.67
## GAPDH                    64730       0.284    25728.50      90458.83
## ACTB                     63054       0.189    14693.25      77747.08
## PKM                      49623       0.254    16907.00      66529.58
## ACTG1                    48854       0.200    12176.50      61030.50
## TPT1                     44349       0.252    14955.25      59304.58
## APP                      43083       0.205    11095.50      54178.33
## ITGB1                    42873       0.172     8891.50      51764.17
```

```
## ITGA3                   42182       0.223    12093.25      54275.08
## CD24                    41714       0.216    11462.00      53175.58
## FTL                     40830       0.414    28790.25      69619.75
## ENO1                    39477       0.180     8674.75      48151.50
## FTH1                    34238       0.413    24129.25      58366.92
## AHNAK                   32651       0.112     4135.00      36786.25
## ITM2B                   32607       0.298    13858.25      46465.58
## FN1                     32014       0.579    44045.00      76058.50
## CTSD                    30978       0.301    13351.75      44329.58
## S100A6                  30770       0.092     3111.75      33881.25
## EEF2                    30682       0.335    15444.25      46126.50
##        renal_0 renal_3 renal_6 renal_9 X5_AK125p1_Adh.count
## EEF1A1   90272   38853   34048   31426               239248
## SPP1     65298   79054   80888   77389               127128
## GAPDH    50985   17807   16654   17468                99960
## ACTB     23576   13526   10654   11017                55506
## PKM      24223   14980   14042   14383                44159
## ACTG1    22573    9354    7980    8799                56936
## TPT1     20852   16071   12141   10757                50400
## APP      10122   10025   11406   12829                22980
## ITGB1    13689    7848    7235    6794                35480
## ITGA3    16989   12031    9847    9506                34065
## CD24     15392   10237   10015   10204                32246
## FTL      43755   25884   22577   22945               102383
## ENO1     15733    5745    6459    6762                32386
## FTH1     41911   21204   16988   16414                82156
## AHNAK     6527    2812    3750    3451                11620
## ITM2B    12999   15913   13127   13394                27992
## FN1     110993   30854   19374   14959               106221
## CTSD     14332   11041   12405   15629                37448
## S100A6    6739    2077    1763    1868                15292
## EEF2     26275   14205   11337    9960                61685
##        X6_AK125p1_SPH3d.count X7_AK125p1_SPH6d.count
## EEF1A1                 104936                103173
## SPP1                   145794                164672
## GAPDH                   54280                 52301
## ACTB                    44955                 48192
## PKM                     47754                 45858
## ACTG1                   33260                 36404
## TPT1                    45227                 36541
## APP                     34506                 41493
## ITGB1                   25353                 28416
## ITGA3                   37068                 37976
## CD24                    30924                 33000
## FTL                     70698                 76114
## ENO1                    20727                 22796
## FTH1                    56716                 54788
## AHNAK                    9726                 12685
## ITM2B                   43048                 42279
## FN1                     70244                 63233
## CTSD                    40079                 52291
## S100A6                   9160                  9083
## EEF2                    37262                 31831
##        X8_AK125p1_SPH9d.count AK82p2Adh AK82p3SPH3d AK82p3SPH6d
```

```
## EEF1A1                 96223    369732      358958      354492
## SPP1                  168254    207451      271193      405106
## GAPDH                  49922    197908       88206       80886
## ACTB                   41221    141949       84291       93010
## PKM                    41527     98241       83227       80446
## ACTG1                  33062     87108       63832       74141
## TPT1                   31277     70837       73093       68178
## APP                    40545     29785       64443       84487
## ITGB1                  24352     71893       58946       75348
## ITGA3                  31792     66552       67193       67940
## CD24                   31193     32022       61796       88364
## FTL                    70852     54045       86606       74025
## ENO1                   20486    115134       52682       56422
## FTH1                   48194     72329       69510       53322
## AHNAK                  10344     43848       44861       51700
## ITM2B                  39884     25175       59702       69200
## FN1                    41505     62691      181963       76237
## CTSD                   53841     18419       57626       53975
## S100A6                  7603     57942       38977       42301
## EEF2                   28247     51676       54630       45025
##        AK82p3SPH10d AK86p1Adh AK86p2.SPH3d AK86p2.SPH6d AK86p2.SPH10d
## EEF1A1       298852    255621       339466       310284        284038
## SPP1         399705    149488       264813       374388        252692
## GAPDH         74397    137540        91967        81636         76503
## ACTB          79206     85586        86125        82400         90524
## PKM           73785     36763        84009        77840         84746
## ACTG1         70191     49178        67353        71902         88999
## TPT1          58600     70156        85145        68374         53827
## APP           86396     17193        70066        82498         75748
## ITGB1         61731     39034        57480        68742         74395
## ITGA3         64517     40550        71168        66258         66222
## CD24          86975     22302        62035        78315         78935
## FTL           73476     48715        80936        56773         40814
## ENO1          49390     52554        48857        52189         54195
## FTH1          47670     50331        72315        50154         42918
## AHNAK         46990     27703        48435        58478         75045
## ITM2B         64698     25088        58812        57211         44498
## FN1           43674     27776       127619        38869         72670
## CTSD          62983      8925        57473        47544         41351
## S100A6        44065     52298        35948        37213         56693
## EEF2          43864     34303        67288        53282         44425
```

Write these two top 20 genes being expressed more in diseased as Top 20 up-expressed, and the top 20 genes being expressed less as the Top 20 down-expressed genes as csv files. Also, write the top 20 fold change genes to its own csv file

```
write.csv(Top20_down, 'Down-regulated-20.csv', row.names=TRUE)
write.csv(Top20_up, 'Up-regulated-20.csv', row.names=TRUE)
write.csv(Top20_FC, 'Fold-Change-20.csv', row.names=TRUE)
```

What are the top 20 genes up-regulated in renal disease compared to healthy?

```
Up <- as.data.frame(row.names(Top20_up))
colnames(Up) <- 'Gene'
Up
```

```
##            Gene
## 1          XIST
## 2         CLDN2
## 3         TDRD1
## 4        CDKN1C
## 5         CEBPD
## 6  LOC101928796
## 7           LBP
## 8     LOC389332
## 9           CA9
## 10     B4GALNT4
## 11        IFI27
## 12         NAT8
## 13    OVCH1-AS1
## 14      ANGPTL3
## 15      RARRES1
## 16        CADM3
## 17         PRR7
## 18         FMO1
## 19          PDF
## 20          CFH
```

What are the top 20 genes down-regulated in renal disease compared to healthy?

```
Down <- as.data.frame(row.names(Top20_down))
colnames(Down) <- 'Gene'
Down
```

```
##      Gene
## 1  EEF1A1
## 2    SPP1
## 3   GAPDH
## 4    ACTB
## 5     PKM
## 6   ACTG1
## 7    TPT1
## 8     APP
## 9   ITGB1
## 10  ITGA3
## 11   CD24
## 12    FTL
## 13   ENO1
## 14   FTH1
## 15  AHNAK
```

```
## 16  ITM2B
## 17    FN1
## 18   CTSD
## 19 S100A6
## 20   EEF2
```

What are the top 20 genes that have the most fold change in the ratio of healthy to renal disease gene expression? Even the inverse fold change of disease to healthy would

```
FC <- as.data.frame(row.names(Top20_FC))
colnames(FC) <- 'Gene'
FC
```

```
##            Gene
## 1          XIST
## 2     OVCH1-AS1
## 3       LGALS12
## 4      HLA-DQA2
## 5         TDRD1
## 6          AIRN
## 7          CD3D
## 8         CXCR3
## 9     LINC01272
## 10       OR51B2
## 11          SLA
## 12          OXT
## 13 LOC101928796
## 14        CD302
## 15       TDRD12
## 16    LINC00668
## 17       RNASE1
## 18       ABCB11
## 19       ATP2B3
## 20          AVP
```

```
Up$RenalType <- rep('Up',20)
Down$RenalType <- rep('Down',20)
FC$RenalType <- rep('foldChange', 20)
```

```
Up <- Up[order(Up$Gene,decreasing=FALSE),]
FC <- FC[order(FC$Gene,decreasing=FALSE),]
common <- merge(Up,FC, by.x='Gene', by.y='Gene')
```

Common genes to most fold change and up regulated gene expressions are:

```
common
```

```
##           Gene RenalType.x RenalType.y
## 1 LOC101928796          Up  foldChange
## 2    OVCH1-AS1          Up  foldChange
## 3        TDRD1          Up  foldChange
## 4         XIST          Up  foldChange
```

We should go to NCBI Gene get the gene information on these up regulated genes in Renal disease.

```
chr <- as.data.frame(c('21','12','10','X'))
direction <- as.data.frame(c('+','+','+','-'))
start <- as.data.frame(c('45972970','29389294','114174442','73820651'))
end <- as.data.frame(c('45974953','29487324','114232669','73852753'))
TissueMostExpressed <- as.data.frame(c('testis','testis','testis','thyroid'))
fullName <- as.data.frame(c('uncharacterized LOC101928796','OVCH1 antisense RNA 1','tudor domain contai
GeneFunction <- as.data.frame(c('ncRNA.','ncRNA.','protein coding. This gene encodes a protein containi
```

```
info <- cbind(fullName, TissueMostExpressed,GeneFunction, chr,direction, start, end)
colnames(info) <- c('geneName','TissueMostExpressed','geneFunction','chromosome','strandDirection','sta

information <- cbind(common, info)
information
```

```
##           Gene RenalType.x RenalType.y                       geneName
## 1 LOC101928796          Up  foldChange   uncharacterized LOC101928796
## 2    OVCH1-AS1          Up  foldChange          OVCH1 antisense RNA 1
## 3        TDRD1          Up  foldChange      tudor domain containing 1
## 4         XIST          Up  foldChange X inactive specific transcript
##   TissueMostExpressed
## 1              testis
## 2              testis
## 3              testis
## 4             thyroid
##
## 1
## 2
## 3
## 4 ncRNA. X inactivation is an early developmental process in mammalian females that transcriptionally
##   chromosome strandDirection   startBP     endBP
## 1         21               +  45972970  45974953
## 2         12               +  29389294  29487324
## 3         10               + 114174442 114232669
## 4          X               -  73820651  73852753
```

Read in a table of the gene summaries for these genes with some summaries missing for certain genes in the up/down/fold change top 20 genes

```
summaries <- read.csv('GeneDescriptionsNCBIgene.csv', sep=',',header=TRUE,
                      na.strings=c('',' ','NA'))
summaries <- summaries[,c(1:3)]
```

The gene summaries by complete cases

```
summ <- summaries[complete.cases(summaries$geneFunction),]
```

Merge the up, down, and fold change genes with their gene summaries

```
Top20_up$gene <- row.names(Top20_up)
Top20_down$gene <- row.names(Top20_down)
Top20_FC$gene <- row.names(Top20_FC)

up_summ <- merge(summ, Top20_up, by.x='gene',by.y='gene')
down_summ <- merge(summ, Top20_down, by.x='gene',by.y='gene')
fc_summ <- merge(summ, Top20_FC, by.x='gene',by.y='gene')
```

Use lemmatization on the available top 20 down regulated gene summaries

```
library(tm)
library(SnowballC)
library(wordcloud)
library(ggplot2)
library(textstem)
```

```
lemma <- lemmatize_strings(up_summ$geneFunction, dictionary=lexicon::hash_lemmas)

Lemma <- as.data.frame(lemma)
Lemma <- cbind(Lemma, up_summ)

colnames(Lemma)[1] <- 'lemmatized_summary'

write.csv(Lemma, 'Lemmatized_upreg20.csv', row.names=FALSE)
```

```
dir.create('./upreg20-Lemma')

ea <- as.character(Lemma$lemmatized_summary)
setwd('./upreg20-Lemma')

for (j in 1:length(ea)){
  write(ea[j], paste(paste('up',j, sep='.'), '.txt', sep=''))
}
setwd('../')
```

```
KidneyDisease <- Corpus(DirSource("upreg20-Lemma"))

KidneyDisease
```

```
## <<SimpleCorpus>>
## Metadata:  corpus specific: 1, document level (indexed): 0
## Content:  documents: 16
```

```
KidneyDisease <- tm_map(KidneyDisease, removePunctuation)
KidneyDisease <- tm_map(KidneyDisease, removeNumbers)
KidneyDisease <- tm_map(KidneyDisease, tolower)
KidneyDisease <- tm_map(KidneyDisease, removeWords, stopwords("english"))
KidneyDisease <- tm_map(KidneyDisease, stripWhitespace)

dtmKidneyDisease <- DocumentTermMatrix(KidneyDisease)
dtmKidneyDisease
```

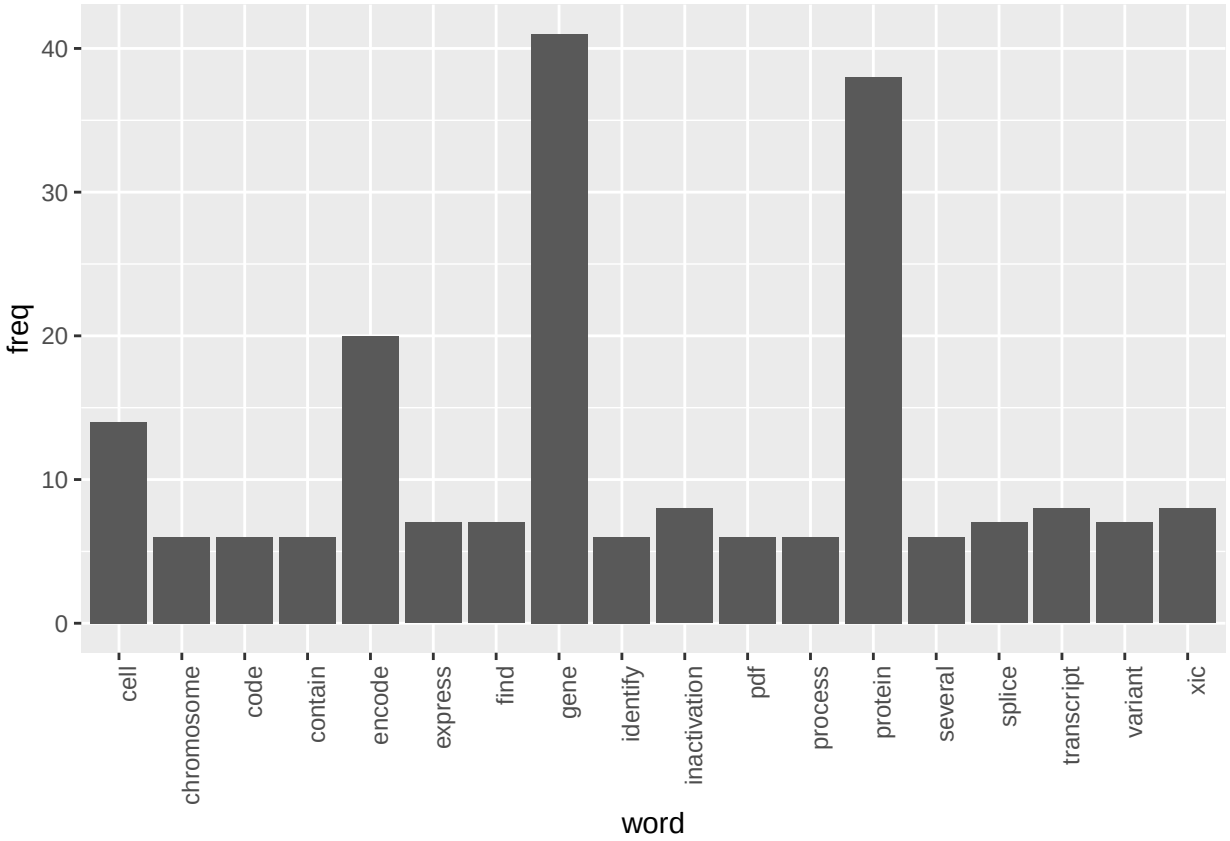
```
## <<DocumentTermMatrix (documents: 16, terms: 398)>>
## Non-/sparse entries: 667/5701
## Sparsity           : 90%
## Maximal term length: 23
## Weighting          : term frequency (tf)
```

```
freq <- colSums(as.matrix(dtmKidneyDisease))

FREQ <- data.frame(freq)
ord <- order(freq, decreasing=TRUE)

freq[head(ord, 25)]
```

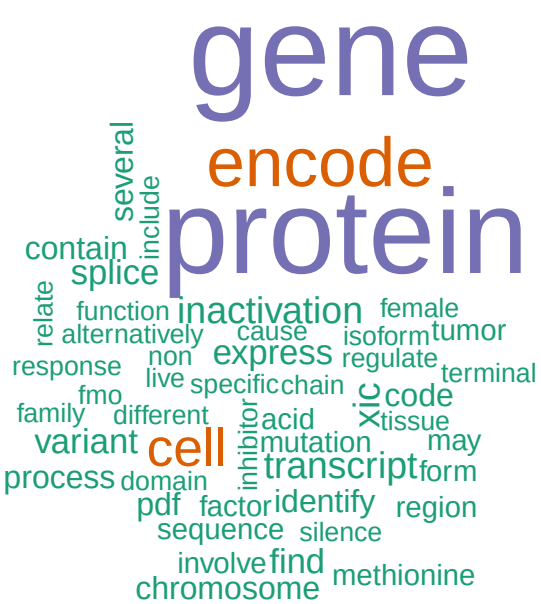
```
##         gene      protein       encode         cell   transcript
##           41           38           20           14            8
## inactivation          xic      express         find       splice
##            8            8            7            7            7
##      variant      contain      process          pdf     identify
##            7            6            6            6            6
##   chromosome         code      several      involve          may
##            6            6            6            5            5
##     mutation         acid     sequence   methionine       factor
##            5            5            5            5            5
```

Up regulated genes

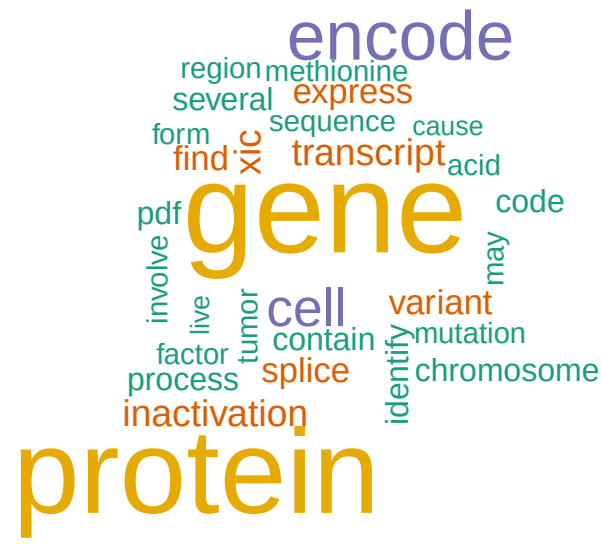
```
wf <- data.frame(word=names(freq), freq=freq)
p <- ggplot(subset(wf, freq>5), aes(word, freq))
p <- p + geom_bar(stat= 'identity')
p <- p + theme(axis.text.x=element_text(angle=90, hjust=1))
p
```




```
wordcloud(names(freq), freq, min.freq=4,colors=brewer.pal(3,'Dark2'))
```




```
wordcloud(names(freq), freq, max.words=30,colors=brewer.pal(6,'Dark2'))
```



Now for the down regulated available summaries for the top 20 down regulated genes

```
lemma <- lemmatize_strings(down_summ$geneFunction, dictionary=lexicon::hash_lemmas)

Lemma <- as.data.frame(lemma)
Lemma <- cbind(Lemma, down_summ)

colnames(Lemma)[1] <- 'lemmatized_summary'

write.csv(Lemma, 'Lemmatized_downreg20.csv', row.names=FALSE)
```

```
dir.create('./downreg20-Lemma')

ea <- as.character(Lemma$lemmatized_summary)
setwd('./downreg20-Lemma')

for (j in 1:length(ea)){
  write(ea[j], paste(paste('down',j, sep='.'), '.txt', sep=''))
}
setwd('../')
```

```
KidneyDisease <- Corpus(DirSource("downreg20-Lemma"))

KidneyDisease
```

```
## <<SimpleCorpus>>
## Metadata:  corpus specific: 1, document level (indexed): 0
## Content:  documents: 20
```

```
KidneyDisease <- tm_map(KidneyDisease, removePunctuation)
KidneyDisease <- tm_map(KidneyDisease, removeNumbers)
KidneyDisease <- tm_map(KidneyDisease, tolower)
KidneyDisease <- tm_map(KidneyDisease, removeWords, stopwords("english"))
KidneyDisease <- tm_map(KidneyDisease, stripWhitespace)

dtmKidneyDisease <- DocumentTermMatrix(KidneyDisease)
dtmKidneyDisease
```

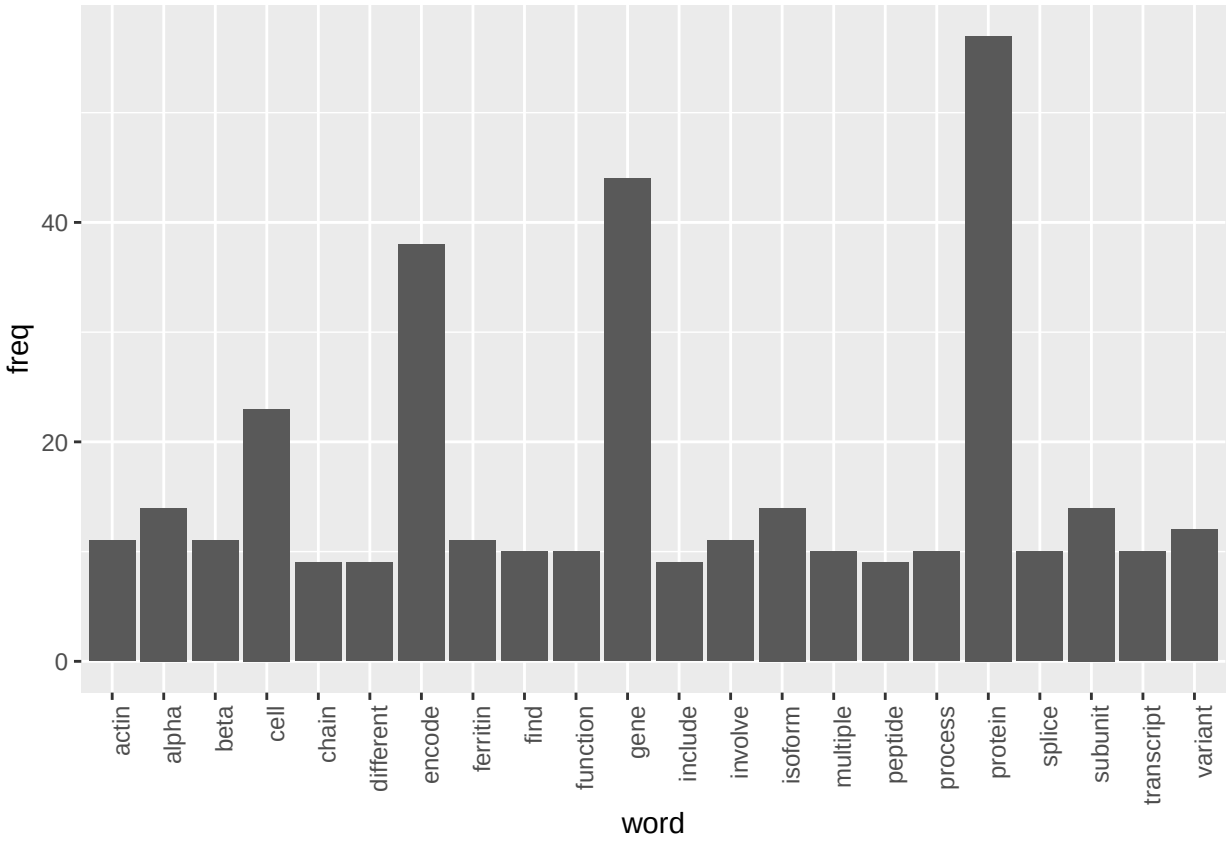
```
## <<DocumentTermMatrix (documents: 20, terms: 501)>>
## Non-/sparse entries: 940/9080
## Sparsity           : 91%
## Maximal term length: 20
## Weighting          : term frequency (tf)
```

```
freq <- colSums(as.matrix(dtmKidneyDisease))

FREQ <- data.frame(freq)
ord <- order(freq, decreasing=TRUE)

freq[head(ord, 25)]
```

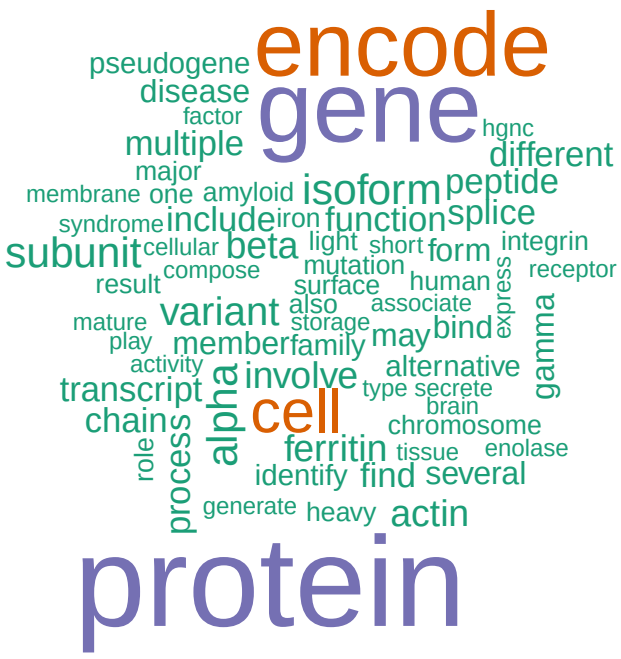
```
##    protein       gene     encode       cell    isoform    subunit
##         57         44         38         23         14         14
##      alpha    variant      actin    involve   ferritin       beta
##         14         12         11         11         11         11
##    process     splice transcript   function   multiple       find
##         10         10         10         10         10         10
##  different    include      chain    peptide       form    disease
##          9          9          9          9          8          8
##        may
##          8
```

Down regulated

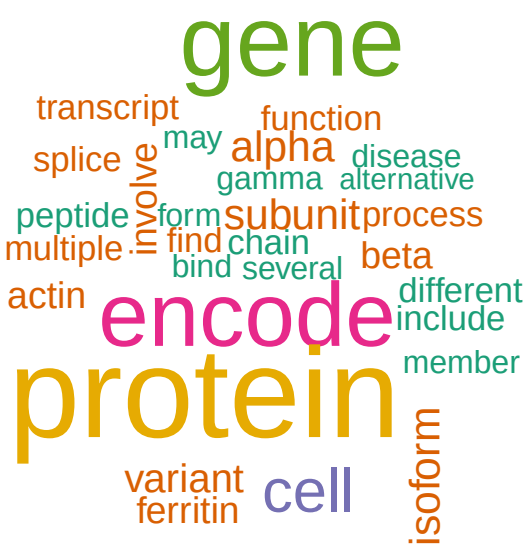
```
wf <- data.frame(word=names(freq), freq=freq)
p <- ggplot(subset(wf, freq>8), aes(word, freq))
p <- p + geom_bar(stat= 'identity')
p <- p + theme(axis.text.x=element_text(angle=90, hjust=1))
p
```




```
wordcloud(names(freq), freq, min.freq=4,colors=brewer.pal(3,'Dark2'))
```




```
wordcloud(names(freq), freq, max.words=30,colors=brewer.pal(6,'Dark2'))
```



Now for the fold change top 20 available gene summaries

```
lemma <- lemmatize_strings(fc_summ$geneFunction, dictionary=lexicon::hash_lemmas)

Lemma <- as.data.frame(lemma)
Lemma <- cbind(Lemma, fc_summ)

colnames(Lemma)[1] <- 'lemmatized_summary'

write.csv(Lemma, 'Lemmatized_fcreg20.csv', row.names=FALSE)
```

```
dir.create('./fcreg20-Lemma')

ea <- as.character(Lemma$lemmatized_summary)
setwd('./fcreg20-Lemma')

for (j in 1:length(ea)){
  write(ea[j], paste(paste('fc',j, sep='.'), '.txt', sep=''))
}
setwd('../')
```

```
KidneyDisease <- Corpus(DirSource("fcreg20-Lemma"))

KidneyDisease
```

```
## <<SimpleCorpus>>
## Metadata:  corpus specific: 1, document level (indexed): 0
## Content:  documents: 16
```

```
KidneyDisease <- tm_map(KidneyDisease, removePunctuation)
KidneyDisease <- tm_map(KidneyDisease, removeNumbers)
KidneyDisease <- tm_map(KidneyDisease, tolower)
KidneyDisease <- tm_map(KidneyDisease, removeWords, stopwords("english"))
KidneyDisease <- tm_map(KidneyDisease, stripWhitespace)

dtmKidneyDisease <- DocumentTermMatrix(KidneyDisease)
dtmKidneyDisease
```

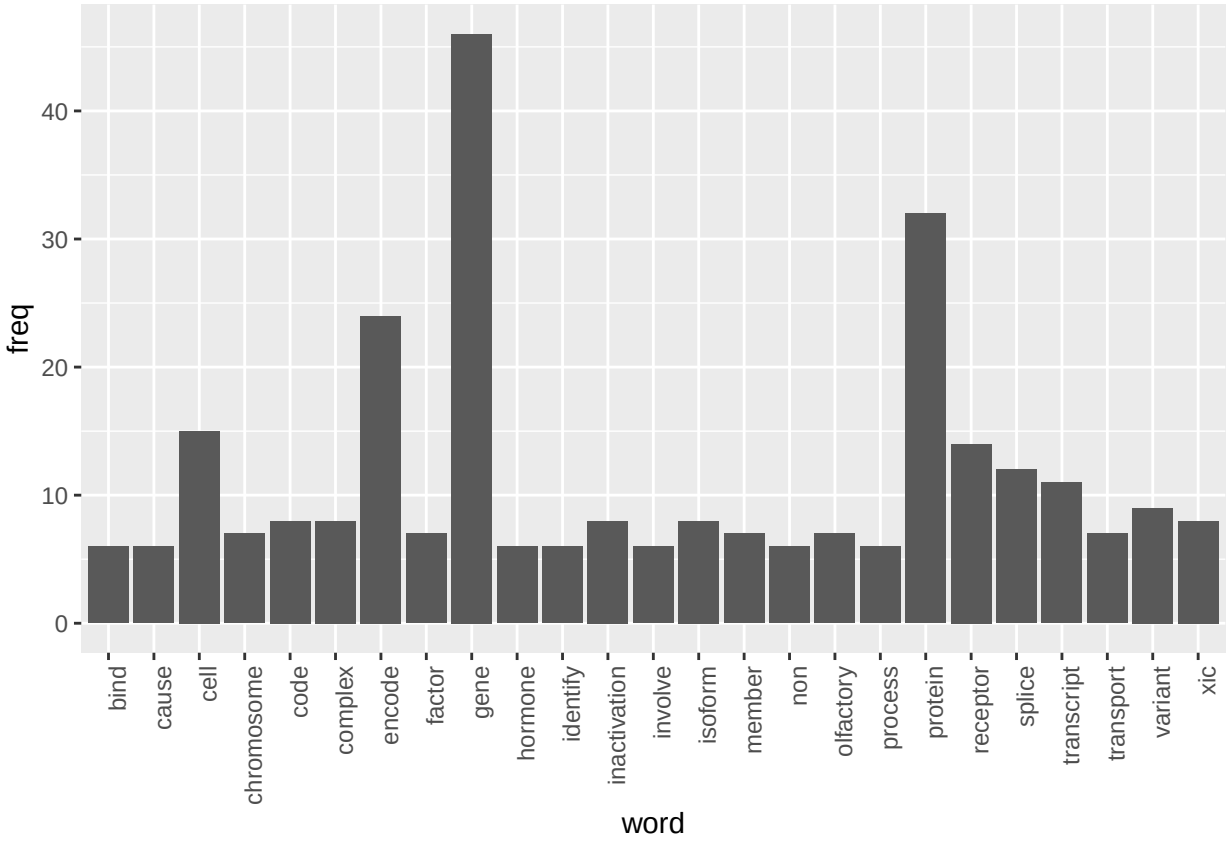
```
## <<DocumentTermMatrix (documents: 16, terms: 415)>>
## Non-/sparse entries: 728/5912
## Sparsity           : 89%
## Maximal term length: 17
## Weighting          : term frequency (tf)
```

```
freq <- colSums(as.matrix(dtmKidneyDisease))

FREQ <- data.frame(freq)
ord <- order(freq, decreasing=TRUE)

freq[head(ord, 25)]
```

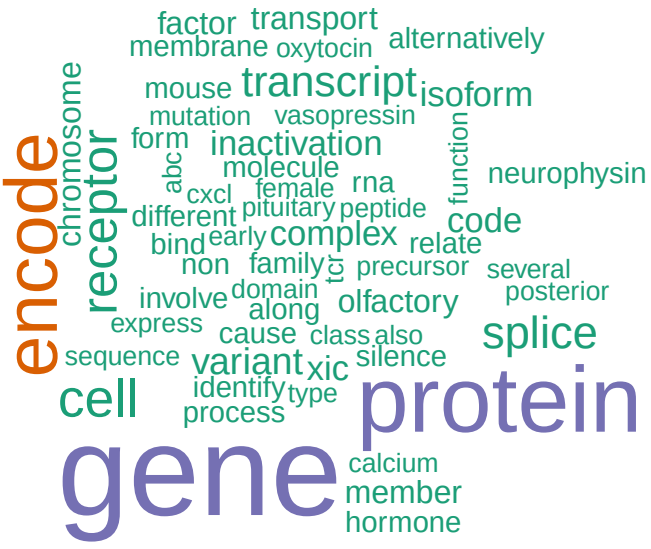
```
##         gene      protein       encode         cell     receptor
##           46           32           24           15           14
##       splice   transcript      variant         code      complex
##           12           11            9            8            8
## inactivation          xic      isoform       member    transport
##            8            8            8            7            7
##    olfactory       factor   chromosome         bind        cause
##            7            7            7            6            6
##      involve      hormone          non      process     identify
##            6            6            6            6            6
```

Fold Change genes

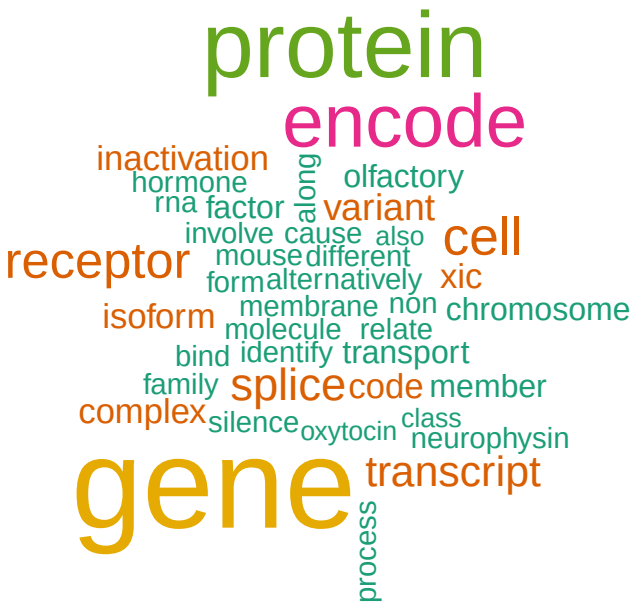
```
wf <- data.frame(word=names(freq), freq=freq)
p <- ggplot(subset(wf, freq>5), aes(word, freq))
p <- p + geom_bar(stat= 'identity')
p <- p + theme(axis.text.x=element_text(angle=90, hjust=1))
p
```




```
wordcloud(names(freq), freq, min.freq=4,colors=brewer.pal(3,'Dark2'))
```




```
wordcloud(names(freq), freq, max.words=40,colors=brewer.pal(6,'Dark2'))
```



This script takes articles from the abstracts on Kidney Disease articles from NCBI's PubMed, PLOS, and the summary of the NCBI GEO sample pages

This creates a directory to stem the abstracts and preprocess from the csv file into a corpus of 20 files in a folder called KidneyDisease.

```
Auto <- read.csv('NIH_PLOS_articles_kidney_disease.csv', sep=',',
                 header=FALSE, na.strings=c('',' '))
```

```
colnames(Auto) <- c('abstract','source')
auto <- Auto[complete.cases(Auto$abstract),]


dir.create('./KidneyDisease')

ea <- as.character(auto$abstract)
setwd('./KidneyDisease')

for (j in 1:length(ea)){
  write(ea[j], paste(paste('EA',j, sep='.'), '.txt', sep=''))
}
setwd('../')
```

This code preprocesses and stems the corpus

```
KidneyDisease <- Corpus(DirSource("KidneyDisease"))


KidneyDisease
```

```
## <<SimpleCorpus>>
## Metadata:  corpus specific: 1, document level (indexed): 0
## Content:  documents: 43
```

```
#KidneyDisease <- tm_map(KidneyDisease, removePunctuation)
#KidneyDisease <- tm_map(KidneyDisease, removeNumbers)
KidneyDisease <- tm_map(KidneyDisease, tolower)
KidneyDisease <- tm_map(KidneyDisease, removeWords, stopwords("english"))
KidneyDisease <- tm_map(KidneyDisease, stripWhitespace)
KidneyDisease <- tm_map(KidneyDisease, stemDocument)

dtmKidneyDisease <- DocumentTermMatrix(KidneyDisease)

freq <- colSums(as.matrix(dtmKidneyDisease))
```

This code orders words stemmed by frequency and finds input correlations

```
FREQ <- data.frame(freq)
ord <- order(freq, decreasing=TRUE)

freq[head(ord, 25)]
```

```
##     kidney     medium     associ       cell      serum supplement
##        223        128        112        110        102         98
##     sodium   concentr     diseas    univers       egfr     depart
##         97         82         77         77         75         74
##     declin        use    purchas   function      renal  medicine,
##         71         68         64         64         63         61
##      sampl       risk     growth      incid      tissu      rapid
##         57         54         51         51         50         50
##        san
##         50
```

```
findAssocs(dtmKidneyDisease, "renal", corlimit=0.5)
```

```
## $renal
##             mice           calcul              (b)              .e.
##             0.70             0.69             0.68             0.68
##       accomplish             area            area.        ascertain
##             0.68             0.68             0.68             0.68
##              axi            axial            axis,          biochem
##             0.68             0.68             0.68             0.68
##          biopsy.              can        ckd-relat         collagen
##             0.68             0.68             0.68             0.68
##         content,         content.            coron          deposit
##             0.68             0.68             0.68             0.68
```

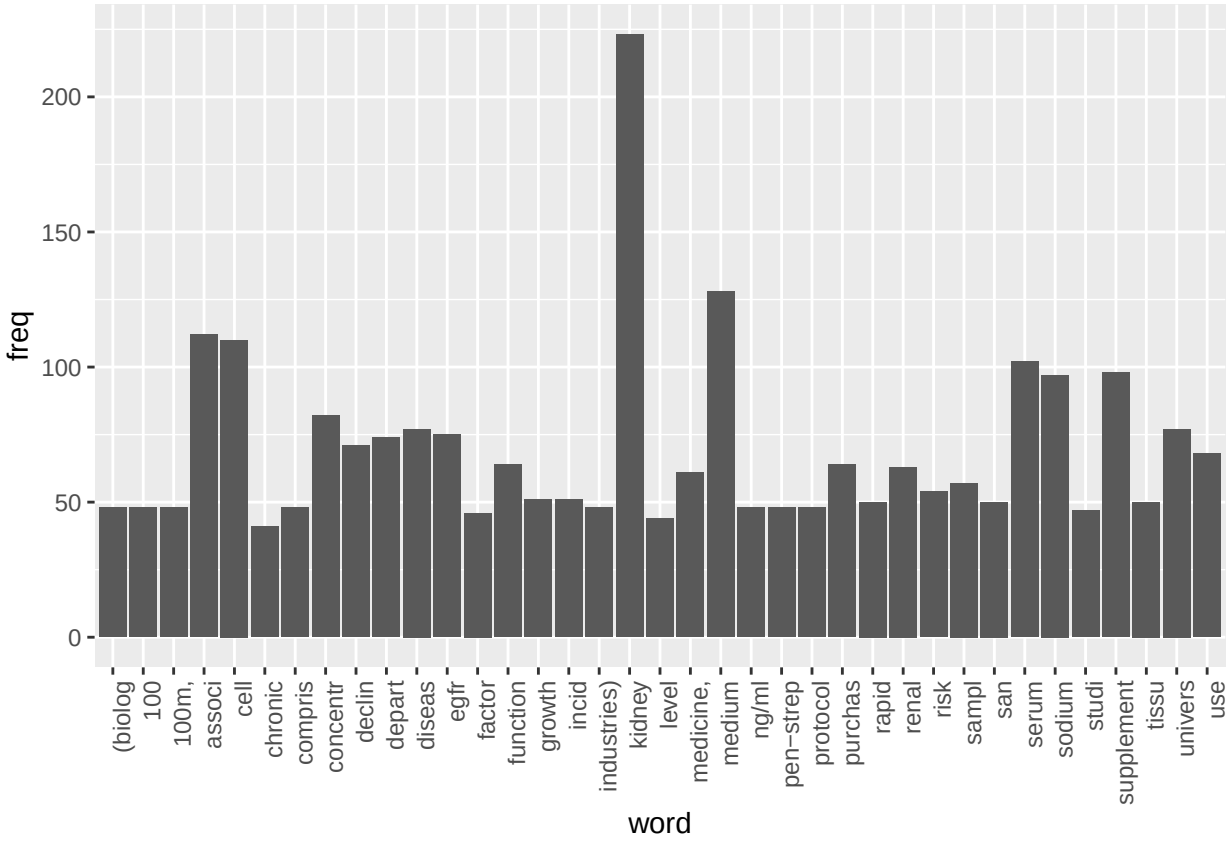
```
##        distance,           easili           ellips        ellipsoid
##             0.68             0.68             0.68             0.68
##           extend           extent          formula             imag
##             0.68             0.68             0.68             0.68
##       interstiti        invasive,             just             make
##             0.68             0.68             0.68             0.68
##            minor         noninvas              now            often
##             0.68             0.68             0.68             0.68
##           organ.        parenchym            pelvi      picrosirius
##             0.68             0.68             0.68             0.68
##            polar              red           remark           risky,
##             0.68             0.68             0.68             0.68
##             scar        scarring,             size            size,
##             0.68             0.68             0.68             0.68
##          sometim            stain         techniqu            today
##             0.68             0.68             0.68             0.68
##           treat             true tubulointerstiti      ultrasound,
##             0.68             0.68             0.68             0.68
##       underestim              via           visual            major
##             0.68             0.68             0.68             0.65
##           obtain           involv
##             0.52             0.51
```

```
findAssocs(dtmKidneyDisease, "pain", corlimit=0.69)
```

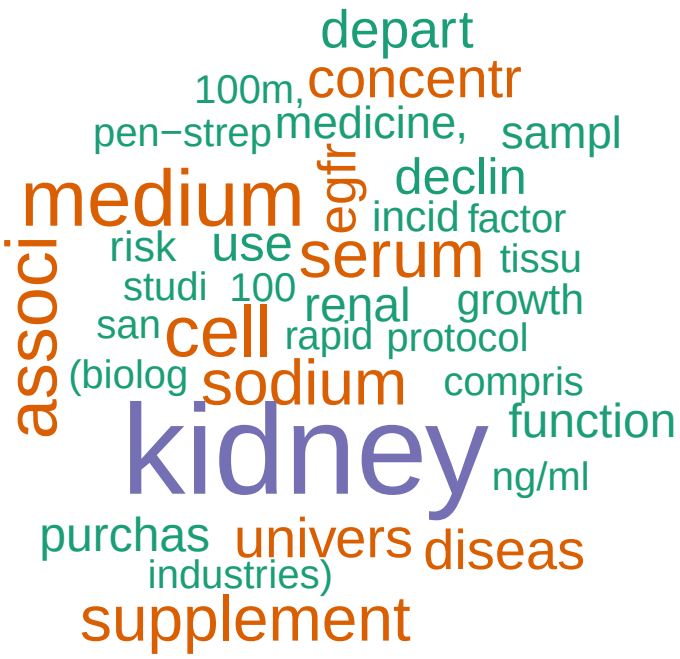
```
## $pain
##             (12)       (23.0-28.0            (25%)            (92%)
##              0.7              0.7              0.7              0.7
##          (health  (sd)ml/min/1.73       0.13-0.97)       0.97-3.07)
##              0.7              0.7              0.7              0.7
##            1.72;              1.9          2-fold             25.2
##              0.7              0.7              0.7              0.7
##              252            70-79              989           [8%])
##              0.7              0.7              0.7              0.7
##             ab9,              abc             abc)           aging,
##              0.7              0.7              0.7              0.7
##           aging;       alkalosis;        analyzer.    anesthesiolog
##              0.7              0.7              0.7              0.7
##        bethesda,       california             city,         composit
##              0.7              0.7              0.7              0.7
##             de4,         egfr0.55          elders:           forest
##              0.7              0.7              0.7              0.7
##              fri             give            harri       inception.
##              0.7              0.7              0.7              0.7
##          insight         interven   investigators.            jh12;
##              0.7              0.7              0.7              0.7
##      kritchevski              kv5,             lake            least
##              0.7              0.7              0.7              0.7
##             lf3,             lost            m(2),            mg11,
##              0.7              0.7              0.7              0.7
##            mj10,          mmol/l         mmol/l),         mmol/l.
##              0.7              0.7              0.7              0.7
##           newman              pa.              pa;            patel
##              0.7              0.7              0.7              0.7
```

```
##         persons.      pittsburgh,         predomin     progression,
##              0.7              0.7              0.7              0.7
##           ratio.             rh6,           rifkin             salt
##              0.7              0.7              0.7              0.7
##             sb8,            separ           sticht             tb7,
##              0.7              0.7              0.7              0.7
##             th2,              ut.            utah,           venous
##              0.7              0.7              0.7              0.7
##             wake       well-funct   winston-salem,         yenchek
##              0.7              0.7              0.7              0.7
##              (b)              .e.       accomplish             area
##              0.7              0.7              0.7              0.7
##            area.        ascertain              axi            axial
##              0.7              0.7              0.7              0.7
##            axis,          biochem          biopsy.              can
##              0.7              0.7              0.7              0.7
##        ckd-relat         collagen         content,         content.
##              0.7              0.7              0.7              0.7
##            coron          deposit        distance,           easili
##              0.7              0.7              0.7              0.7
##           ellips        ellipsoid           extend           extent
##              0.7              0.7              0.7              0.7
##          formula             imag       interstiti        invasive,
##              0.7              0.7              0.7              0.7
##             just             make            minor         noninvas
##              0.7              0.7              0.7              0.7
##              now            often           organ.        parenchym
##              0.7              0.7              0.7              0.7
##            pelvi      picrosirius            polar              red
##              0.7              0.7              0.7              0.7
##           remark           risky,             scar        scarring,
##              0.7              0.7              0.7              0.7
##             size            size,          sometim            stain
##              0.7              0.7              0.7              0.7
##         techniqu            today            treat             true
##              0.7              0.7              0.7              0.7
## tubulointerstiti      ultrasound,       underestim              via
##              0.7              0.7              0.7              0.7
##           visual
##              0.7
```

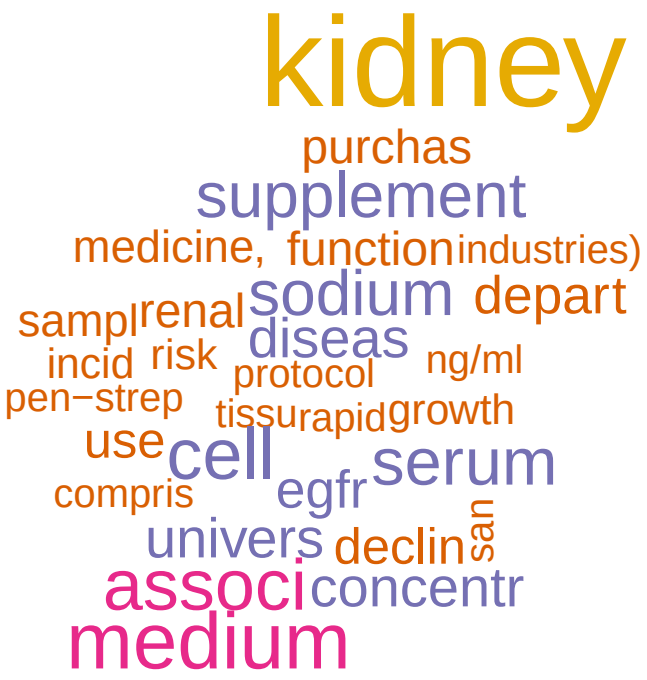
```
wf <- data.frame(word=names(freq), freq=freq)
p <- ggplot(subset(wf, freq>40), aes(word, freq))
p <- p + geom_bar(stat= 'identity')
p <- p + theme(axis.text.x=element_text(angle=90, hjust=1))
p
```




```
wordcloud(names(freq), freq, min.freq=45,colors=brewer.pal(3,'Dark2'))
```




```
wordcloud(names(freq), freq, max.words=30,colors=brewer.pal(6,'Dark2'))
```



The above stemmed the corpus, this will lemmatize the original csv file

and add the field to the table and write out to csv, followed by plot the word count frequencies that were lemmatized and the word clouds

```
#library(textstem)

lemma <- lemmatize_strings(auto$abstract, dictionary=lexicon::hash_lemmas)

Lemma <- as.data.frame(lemma)
Lemma <- cbind(Lemma, auto)

colnames(Lemma) <- c('lemmatizedAbstract','abstract', 'source')

write.csv(Lemma, 'LemmatizedKidneyDisease.csv', row.names=FALSE)
```

```
dir.create('./KidneyDisease-Lemma')

ea <- as.character(Lemma$lemmatizedAbstract)
setwd('./KidneyDisease-Lemma')

for (j in 1:length(ea)){
  write(ea[j], paste(paste('EAL',j, sep='.'), '.txt', sep=''))
}
setwd('../')
```

```
KidneyDisease <- Corpus(DirSource("KidneyDisease-Lemma"))

KidneyDisease
```

```
## <<SimpleCorpus>>
## Metadata:  corpus specific: 1, document level (indexed): 0
## Content:  documents: 43
```

```
#KidneyDisease <- tm_map(KidneyDisease, removePunctuation)
#KidneyDisease <- tm_map(KidneyDisease, removeNumbers)
KidneyDisease <- tm_map(KidneyDisease, tolower)
KidneyDisease <- tm_map(KidneyDisease, removeWords, stopwords("english"))
KidneyDisease <- tm_map(KidneyDisease, stripWhitespace)

dtmKidneyDisease <- DocumentTermMatrix(KidneyDisease)
dtmKidneyDisease
```

```
## <<DocumentTermMatrix (documents: 43, terms: 2418)>>
## Non-/sparse entries: 7417/96557
## Sparsity           : 93%
## Maximal term length: 116
## Weighting          : term frequency (tf)
```

```
freq <- colSums(as.matrix(dtmKidneyDisease))

FREQ <- data.frame(freq)
ord <- order(freq, decreasing=TRUE)

freq[head(ord, 25)]
```

```
##     kidney       cell     medium      serum     sodium supplement
##        223        142        128        102         97         96
##       egfr        100 invitrogen    disease university department
##         93         80         80         78         77         74
##    decline        use   function        4mg    aldrich biological
##         71         67         65         64         64         64
##   industry       poly   purchase        sfm      sigma      renal
##         64         64         64         64         64         63
##  associate
##         62
```

```
pain <- as.data.frame(findAssocs(dtmKidneyDisease, "pain", corlimit=0.99))

kidney <- as.data.frame(findAssocs(dtmKidneyDisease, "kidney", corlimit=0.65))


treatment <- as.data.frame(findAssocs(dtmKidneyDisease, "treatment", corlimit=0.81))

pain
```

```
##                pain
```

```
## 1.9              1
## 23.              1
## 25.2             1
## 252              1
## 28.              1
## 72;              1
## 989              1
## ab9,             1
## abc              1
## age;             1
## alkalosis;       1
## analyzer.        1
## anesthesiology   1
## arterial         1
## arterialized     1
## bethesda,        1
## california       1
## city,            1
## collaborator     1
## collection       1
## composition      1
## de4,             1
## egfr0.55         1
## elder            1
## elder:           1
## forest           1
## fry              1
## give             1
## harris           1
## inception.       1
## insight          1
## intervene        1
## investigator.    1
## jh12;            1
## kritchevsky      1
## kv5,             1
## lake             1
## less             1
## lf3,             1
## lose             1
## mg11,            1
## mj10,            1
## mmol             1
## newman           1
## pa.              1
## pa;              1
## patel            1
## person.          1
## pittsburgh,      1
## predominantly    1
## prevalent        1
## progression,     1
## ratio.           1
## rh6,             1
```

```
## rifkin            1
## salem,            1
## salt              1
## sb8,              1
## separate          1
## sticht            1
## tb7,              1
## th2,              1
## ut.               1
## utah,             1
## venous            1
## wake              1
## winston           1
## yenchek           1
```

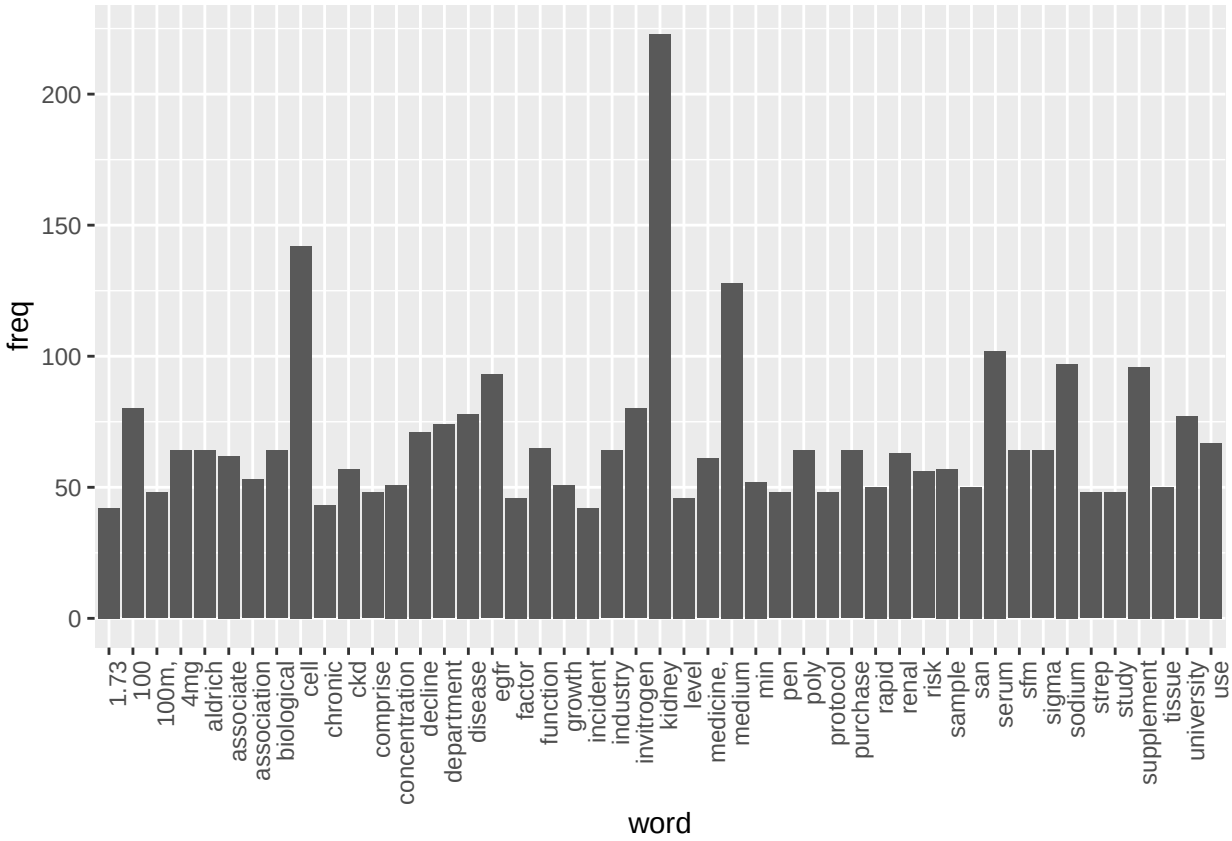
```
kidney
```

```
##             kidney
## function      0.72
## albuminuria   0.67
## ethnic        0.65
## katz          0.65
## washington,   0.65
```

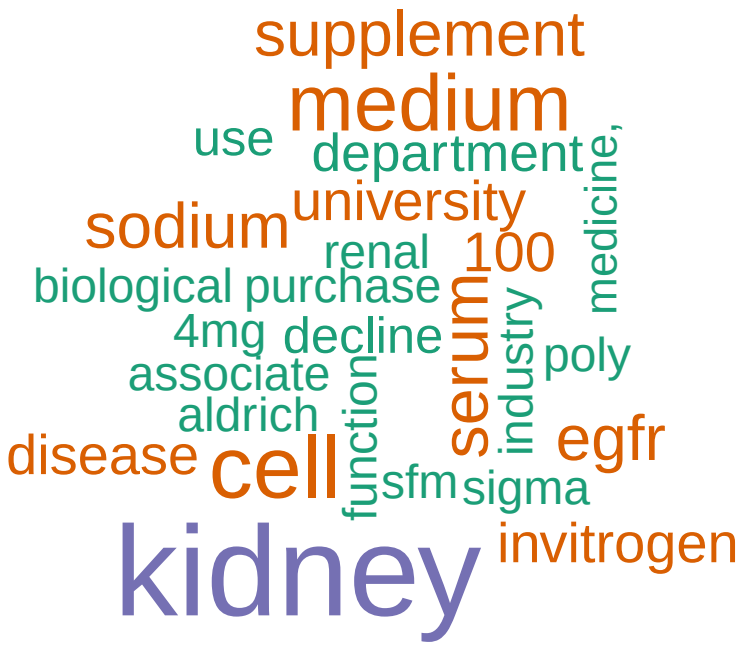
```
treatment
```

```
##       treatment
## cell       0.83
## lipid      0.83
## total      0.83
```

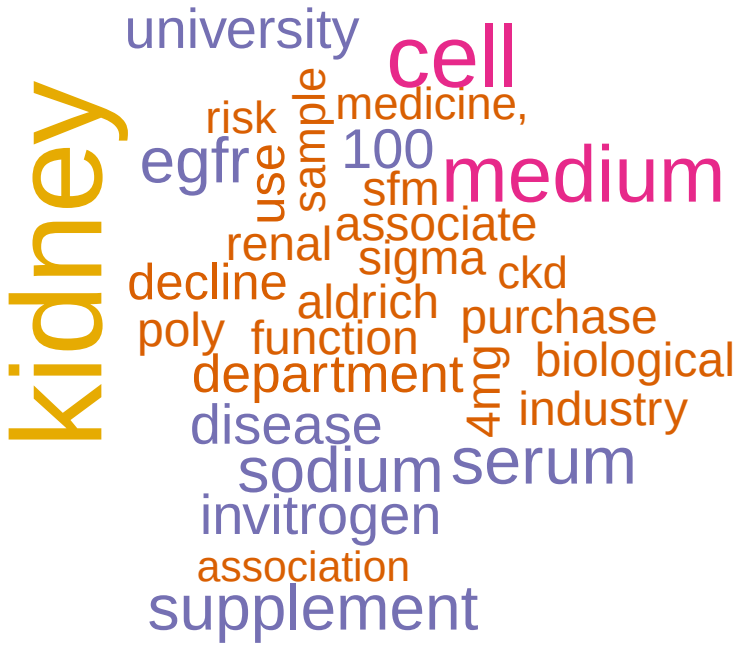
```
wf <- data.frame(word=names(freq), freq=freq)
p <- ggplot(subset(wf, freq>40), aes(word, freq))
p <- p + geom_bar(stat= 'identity')
p <- p + theme(axis.text.x=element_text(angle=90, hjust=1))
p
```




```
wordcloud(names(freq), freq, min.freq=60,colors=brewer.pal(3,'Dark2'))
```




```
wordcloud(names(freq), freq, max.words=30,colors=brewer.pal(6,'Dark2'))
```



Now for some machine learning on predicting renal or kidney type from these samples of 12 healthy and 4 renal disease using the top 20 genes of up/down/fold change genes

```
FC <- Top20_FC[,4:20]
UP <- Top20_up[,5:20]
DOWN <- Top20_down[,5:20]

FC$gene <- row.names(FC)
UP$gene <- row.names(UP)
DOWN$gene <- row.names(DOWN)
```

```
t_tall <- rbind(FC,UP,DOWN)
t_tall <- t_tall[!duplicated(t_tall$gene),]
```

#remove the statistical observations

```
t_tall <- t(t_tall)
row.names(t_tall)
```

```
##  [1] "renal_0"                "renal_3"
##  [3] "renal_6"                "renal_9"
##  [5] "X5_AK125p1_Adh.count"   "X6_AK125p1_SPH3d.count"
##  [7] "X7_AK125p1_SPH6d.count" "X8_AK125p1_SPH9d.count"
```

```
##  [9] "AK82p2Adh"              "AK82p3SPH3d"
## [11] "AK82p3SPH6d"            "AK82p3SPH10d"
## [13] "AK86p1Adh"              "AK86p2.SPH3d"
## [15] "AK86p2.SPH6d"           "AK86p2.SPH10d"
## [17] "gene"
```

```
dim(t_tall)
```

```
## [1] 17 56
```

```
t_tall <- t_tall[1:16,] #remove gene row
```

```
renal2 <- as.data.frame(rep('renal disease',4))
healthy2 <- as.data.frame(rep('healthy',12))
colnames(renal2) <- 'type'
colnames(healthy2) <- 'type'

type <- rbind(renal2, healthy2)

ML_set <- cbind(type,t_tall)
dim(ML_set)
```

```
## [1] 16 57
```

```
ML_set2 <- ML_set[,2:57]

for (i in 1:ncol(ML_set2)){
        ML_set2[,i] <- as.numeric(as.character(ML_set2[,i]))
}

ML_set2$type <- ML_set$type
ML_set <- ML_set2[,c(57,1:56)]
```

The data set that will be used for Machine Learning will predict if the sample is renal disease or healthy. The samples will have to be randomized into 80% train and 20% test

```
library(caret)
library(randomForest)
library(MASS)
library(gbm)
library(dplyr)
```

```
set.seed(189678345)
```

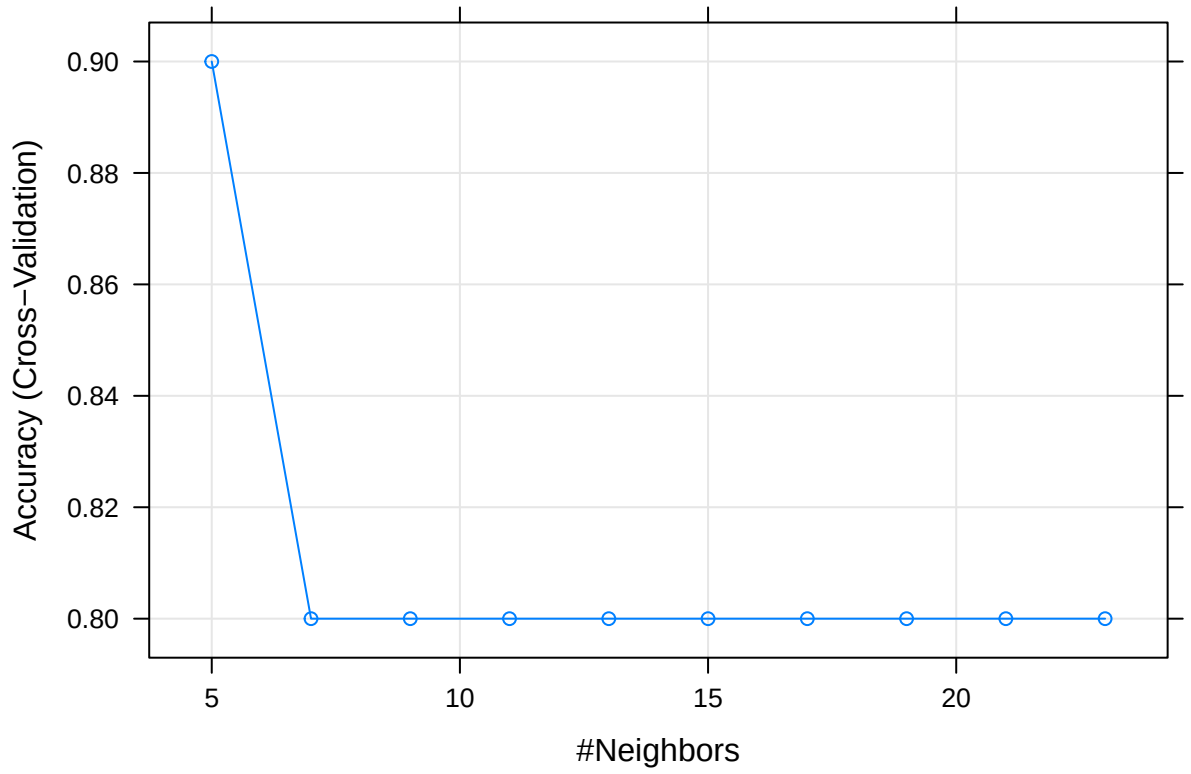
```
inTrain <- createDataPartition(y=ML_set$type, p=0.8, list=FALSE)

trainingSet <- ML_set[inTrain,]
testingSet <- ML_set[-inTrain,]
```

KNN

```
system.time(knnMod <- train(type  ~ .,
                method='knn', preProcess=c('center','scale'),
                tuneLength=10, trControl=trainControl(method='cv'), data=trainingSet))
```

```
##    user  system elapsed
##    2.53    0.08    2.84
```

```
plot(knnMod)
```



The predicted results with KNN

```
predKNN <- predict(knnMod, testingSet)
predKNN
```

```
## [1] healthy healthy
## Levels: renal disease healthy
```

The actual values in the testing set

```
testingSet$type
```

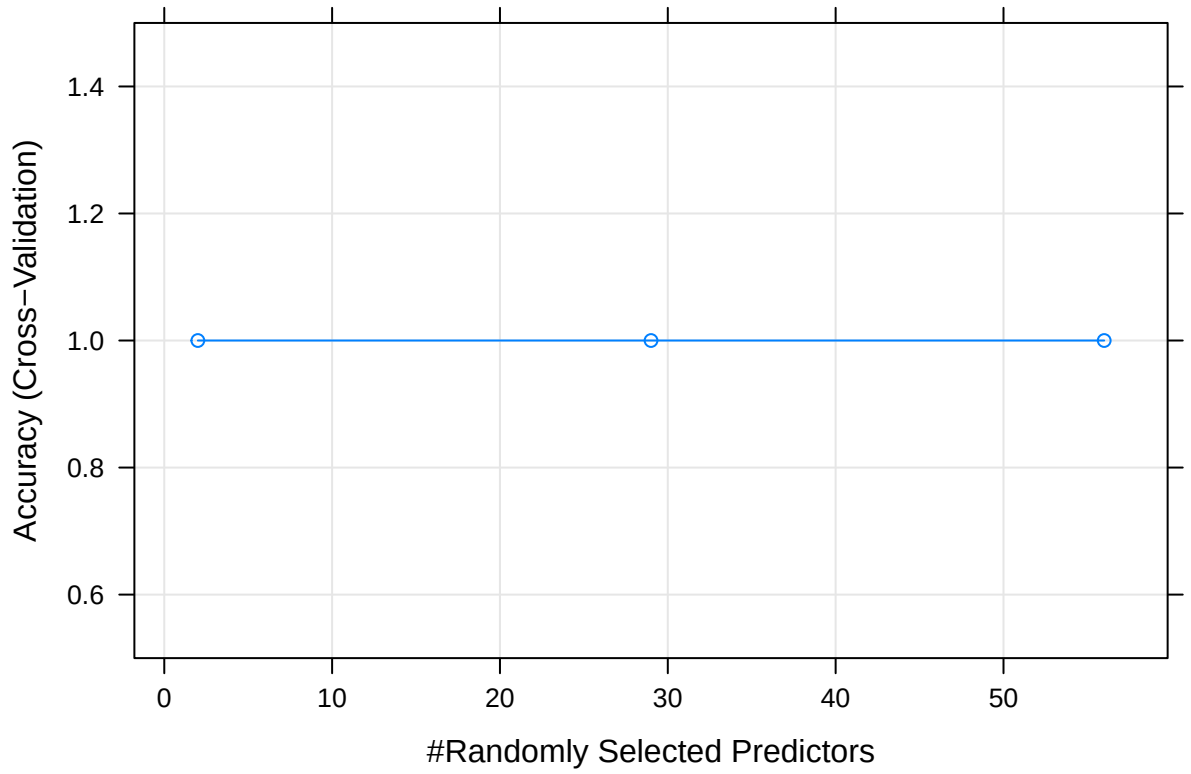
```
## [1] healthy healthy
## Levels: renal disease healthy
```

Random Forest

```
system.time(rfMod <- train(type ~., method='rf', data=(trainingSet),
              trControl=trainControl(method='cv'), number=5))
```

```
##    user  system elapsed
##    1.45    0.09    1.74
```

```
plot(rfMod)
```



The predicted Random Forest results and the actual results

```
predRF <- predict(rfMod, testingSet)
predRF
```

```
## [1] healthy healthy
## Levels: renal disease healthy
```

```
testingSet$type
```

```
## [1] healthy healthy
## Levels: renal disease healthy
```